

RAW SEQUENCE LISTING

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Application Serial Number: 09/852,922C
Source: 1FW/6
Date Processed by STIC: 10/12/06

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IFW16

RAW SEQUENCE LISTING

DATE: 10/12/2006

PATENT APPLICATION: US/09/852,922C

TIME: 14:24:52

Input Set : A:\10089_14 Sequence Listing 1-37 (Oct. 5, 2006).DOC

Output Set: N:\CRF4\10122006\I852922C.raw

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2 <110> APPLICANT: TOYO BOSEKI KABUSHIKI KAISHA
W--> 3 <120> TITLE OF INVENTION: MODIFIED THERMOSTABLE DNA POLYMERASE
W--> 4 <130> FILE REFERENCE: 10089/14
W--> 5 <140> CURRENT APPLICATION NUMBER: US 09/852,922C
6 <141> CURRENT FILING DATE: 2001-05-10
7 <150> PRIOR APPLICATION NUMBER: JP 2000-138796
8 <151> PRIOR FILING DATE: 2000-05-11
W--> 9 <160> NUMBER OF SEQ ID: 37
10 <170> SOFTWARE: PatentIn Ver. 2.1
W--> 11 <210> SEQ ID NO: 1
12 <211> LENGTH: 5342
13 <212> TYPE: DNA
14 <213> ORGANISM: Pyrococcus kodakaraensis
W--> 15 <220> FEATURE:
16 <221> NAME/KEY: CDS
17 <222> LOCATION: (156)..(5165)
18 <223> OTHER INFORMATION: 1374-2453 intron, 2709-4316 intron
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21 gcttgagggc ctgcggttat gggacgttgc agtttgcgcc tactcaaaga tgccggtttt 60
23 ataacggaga aaaatgggga gctattacga tctctccttg atgtgggggtt tacaataaag 120
25 cctggattgt tctacaagat tatgggggat gaaag atg atc ctc gac act gac 173
26                                     Met Ile Leu Asp Thr Asp
27                                     1               5
29 tac ata acc gag gat gga aag cct gtc ata aga att ttc aag aag gaa 221
30 Tyr Ile Thr Glu Asp Gly Lys Pro Val Ile Arg Ile Phe Lys Lys Glu
31               10               15               20
33 aac ggc gag ttt aag att gag tac gac cgg act ttt gaa ccc tac ttc 269
34 Asn Gly Glu Phe Lys Ile Glu Tyr Asp Arg Thr Phe Glu Pro Tyr Phe
35               25               30               35
37 tac gcc ctc ctg aag gac gat tct gcc att gag gaa gtc aag aag ata 317
38 Tyr Ala Leu Leu Lys Asp Asp Ser Ala Ile Glu Glu Val Lys Lys Ile
39               40               45               50
41 acc gcc gag agg cac ggg acg gtt gta acg gtt aag cgg gtt gaa aag 365
42 Thr Ala Glu Arg His Gly Thr Val Val Thr Val Lys Arg Val Glu Lys
43 55               60               65               70
45 gtt cag aag aag ttc ctc ggg aga cca gtt gag gtc tgg aaa ctc tac 413
46 Val Gln Lys Lys Phe Leu Gly Arg Pro Val Glu Val Trp Lys Leu Tyr
47               75               80               85
49 ttt act cat ccg cag gac gtc cca gcg ata agg gac aag ata cga gag 461
50 Phe Thr His Pro Gln Asp Val Pro Ala Ile Arg Asp Lys Ile Arg Glu
51               90               95               100
53 cat ggg gca gtt att gac atc tac gag tac gac ata ccc ttc gcc aag 509
54 His Gly Ala Val Ile Asp Ile Tyr Glu Tyr Asp Ile Pro Phe Ala Lys

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55          105          110          115
57 cgc tac ctc ata gac aag gga tta gtg cca atg gaa ggc gac gag gag 557
58 Arg Tyr Leu Ile Asp Lys Gly Leu Val Pro Met Glu Gly Asp Glu Glu
59      120          125          130
61 ctg aaa atg ctc gcc ttc gac att gaa act ctc tac cat gag ggc gag 605
62 Leu Lys Met Leu Ala Phe Asp Ile Glu Thr Leu Tyr His Glu Gly Glu
63 135          140          145          150
65 gag ttc gcc gag ggg cca atc ctt atg ata agc tac gcc gac gag gaa 653
66 Glu Phe Ala Glu Gly Pro Ile Leu Met Ile Ser Tyr Ala Asp Glu Glu
67      155          160          165
69 ggg gcc agg gtg ata act tgg aag aac gtg gat ctc ccc tac gtt gac 701
70 Gly Ala Arg Val Ile Thr Trp Lys Asn Val Asp Leu Pro Tyr Val Asp
71      170          175          180
73 gtc gtc tcg acg gag agg gag atg ata aag cgc ttc ctc cgt gtt gtg 749
74 Val Val Ser Thr Glu Arg Glu Met Ile Lys Arg Phe Leu Arg Val Val
75      185          190          195
77 aag gag aaa gac ccg gac gtt ctc ata acc tac aac ggc gac aac ttc 797
78 Lys Glu Lys Asp Pro Asp Val Leu Ile Thr Tyr Asn Gly Asp Asn Phe
79      200          205          210
81 gac ttc gcc tat ctg aaa aag cgc tgt gaa aag ctc gga ata aac ttc 845
82 Asp Phe Ala Tyr Leu Lys Lys Arg Cys Glu Lys Leu Gly Ile Asn Phe
83 215          220          225          230
85 gcc ctc gga agg gat gga agc gag ccg aag att cag agg atg ggc gac 893
86 Ala Leu Gly Arg Asp Gly Ser Glu Pro Lys Ile Gln Arg Met Gly Asp
87      235          240          245
89 agg ttt gcc gtc gaa gtg aag gga cgg ata cac ttc gat ctc tat cct 941
90 Arg Phe Ala Val Glu Val Lys Gly Arg Ile His Phe Asp Leu Tyr Pro
91      250          255          260
93 gtg ata aga cgg acg ata aac ctg ccc aca tac acg ctt gag gcc gtt 989
94 Val Ile Arg Arg Thr Ile Asn Leu Pro Thr Tyr Thr Leu Glu Ala Val
95      265          270          275
97 tat gaa gcc gtc ttc ggt cag ccg aag gag aag gtt tac gct gag gaa 1037
98 Tyr Glu Ala Val Phe Gly Gln Pro Lys Glu Lys Val Tyr Ala Glu Glu
99      280          285          290
101 ata acc aca gcc tgg gaa acc ggc gag aac ctt gag aga gtc gcc cgc 1085
102 Ile Thr Thr Ala Trp Glu Thr Gly Glu Asn Leu Glu Arg Val Ala Arg
103 295          300          305          310
105 tac tcg atg gaa gat gcg aag gtc aca tac gag ctt ggg aag gag ttc 1133
106 Tyr Ser Met Glu Asp Ala Lys Val Thr Tyr Glu Leu Gly Lys Glu Phe
107      315          320          325
109 ctt ccg atg gag gcc cag ctt tct cgc tta atc ggc cag tcc ctc tgg 1181
110 Leu Pro Met Glu Ala Gln Leu Ser Arg Leu Ile Gly Gln Ser Leu Trp
111      330          335          340
113 gac gtc tcc cgc tcc agc act ggc aac ctc gtt gag tgg ttc ctc ctc 1229
114 Asp Val Ser Arg Ser Ser Thr Gly Asn Leu Val Glu Trp Phe Leu Leu
115      345          350          355
117 agg aag gcc tat gag agg aat gag ctg gcc ccg aac aag ccc gat gaa 1277
118 Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala Pro Asn Lys Pro Asp Glu
119      360          365          370

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121	aag	gag	ctg	gcc	aga	aga	cgg	cag	agc	tat	gaa	gga	ggc	tat	gta	aaa	1325
122	Lys	Glu	Leu	Ala	Arg	Arg	Arg	Gln	Ser	Tyr	Glu	Gly	Gly	Tyr	Val	Lys	
123	375						380				385					390	
125	gag	ccc	gag	aga	ggg	ttg	tgg	gag	aac	ata	gtg	tac	cta	gat	ttt	aga	1373
126	Glu	Pro	Glu	Arg	Gly	Leu	Trp	Glu	Asn	Ile	Val	Tyr	Leu	Asp	Phe	Arg	
127					395					400						405	
129	tgc	cat	cca	gcc	gat	acg	aag	gtt	gtc	gtc	aag	ggg	aag	ggg	att	ata	1421
130	Cys	His	Pro	Ala	Asp	Thr	Lys	Val	Val	Val	Lys	Gly	Lys	Gly	Ile	Ile	
131				410						415						420	
133	aac	atc	agc	gag	gtt	cag	gaa	ggg	gac	tat	gtc	ctt	ggg	att	gac	ggc	1469
134	Asn	Ile	Ser	Glu	Val	Gln	Glu	Gly	Asp	Tyr	Val	Leu	Gly	Ile	Asp	Gly	
135			425					430					435				
137	tgg	cag	aga	gtt	aga	aaa	gta	tgg	gaa	tac	gac	tac	aaa	ggg	gag	ctt	1517
138	Trp	Gln	Arg	Val	Arg	Lys	Val	Trp	Glu	Tyr	Asp	Tyr	Lys	Gly	Glu	Leu	
139	440						445						450				
141	gta	aac	ata	aac	ggg	tta	aag	tgt	acg	ccc	aat	cat	aag	ctt	ccc	gtt	1565
142	Val	Asn	Ile	Asn	Gly	Leu	Lys	Cys	Thr	Pro	Asn	His	Lys	Leu	Pro	Val	
143	455				460					465						470	
145	gtt	aca	aag	aac	gaa	cga	caa	acg	aga	ata	aga	gac	agt	ctt	gct	aag	1613
146	Val	Thr	Lys	Asn	Glu	Arg	Gln	Thr	Arg	Ile	Arg	Asp	Ser	Leu	Ala	Lys	
147					475					480						485	
149	tct	ttc	ctt	act	aaa	aaa	gtt	aag	ggc	aag	ata	ata	acc	act	ccc	ctt	1661
150	Ser	Phe	Leu	Thr	Lys	Lys	Val	Lys	Gly	Lys	Ile	Ile	Thr	Thr	Pro	Leu	
151				490					495					500			
153	ttc	tat	gaa	ata	ggc	aga	gcg	aca	agt	gag	aat	att	cca	gaa	gaa	gag	1709
154	Phe	Tyr	Glu	Ile	Gly	Arg	Ala	Thr	Ser	Glu	Asn	Ile	Pro	Glu	Glu	Glu	
155			505					510					515				
157	gtt	ctc	aag	gga	gag	ctc	gct	ggc	ata	cta	ttg	gct	gaa	gga	acg	ctc	1757
158	Val	Leu	Lys	Gly	Glu	Leu	Ala	Gly	Ile	Leu	Leu	Ala	Glu	Gly	Thr	Leu	
159		520					525						530				
161	ttg	agg	aaa	gac	gtt	gaa	tac	ttt	gat	tca	tcc	cgc	aaa	aaa	cgg	agg	1805
162	Leu	Arg	Lys	Asp	Val	Glu	Tyr	Phe	Asp	Ser	Ser	Arg	Lys	Lys	Arg	Arg	
163	535				540						545					550	
165	att	tca	cac	cag	tat	cgt	gtt	gag	ata	acc	att	ggg	aaa	gac	gag	gag	1853
166	Ile	Ser	His	Gln	Tyr	Arg	Val	Glu	Ile	Thr	Ile	Gly	Lys	Asp	Glu	Glu	
167				555						560						565	
169	gag	ttt	agg	gat	cgt	atc	aca	tac	att	ttt	gag	cgt	ttg	ttt	ggg	att	1901
170	Glu	Phe	Arg	Asp	Arg	Ile	Thr	Tyr	Ile	Phe	Glu	Arg	Leu	Phe	Gly	Ile	
171				570						575					580		
173	act	cca	agc	atc	tcg	gag	aag	aaa	gga	act	aac	gca	gta	aca	ctc	aaa	1949
174	Thr	Pro	Ser	Ile	Ser	Glu	Lys	Lys	Gly	Thr	Asn	Ala	Val	Thr	Leu	Lys	
175			585					590					595				
177	gtt	gcg	aag	aag	aat	gtt	tat	ctt	aaa	gtc	aag	gaa	att	atg	gac	aac	1997
178	Val	Ala	Lys	Lys	Asn	Val	Tyr	Leu	Lys	Val	Lys	Glu	Ile	Met	Asp	Asn	
179		600					605						610				
181	ata	gag	tcc	cta	cat	gcc	ccc	tcg	gtt	ctc	agg	gga	ttc	ttc	gaa	ggc	2045
182	Ile	Glu	Ser	Leu	His	Ala	Pro	Ser	Val	Leu	Arg	Gly	Phe	Phe	Glu	Gly	
183	615					620					625					630	
185	gac	ggg	tca	gta	aac	agg	gtt	agg	agg	agt	att	gtt	gca	acc	cag	ggg	2093

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186	Asp	Gly	Ser	Val	Asn	Arg	Val	Arg	Arg	Ser	Ile	Val	Ala	Thr	Gln	Gly	
187					635					640					645		
189	aca	aag	aac	gag	tgg	aag	att	aaa	ctg	gtg	tca	aaa	ctg	ctc	tcc	cag	2141
190	Thr	Lys	Asn	Glu	Trp	Lys	Ile	Lys	Leu	Val	Ser	Lys	Leu	Leu	Ser	Gln	
191				650					655					660			
193	ctt	ggt	atc	cct	cat	caa	acg	tac	acg	tat	cag	tat	cag	gaa	aat	ggg	2189
194	Leu	Gly	Ile	Pro	His	Gln	Thr	Tyr	Thr	Tyr	Gln	Tyr	Gln	Glu	Asn	Gly	
195			665					670					675				
197	aaa	gat	cgg	agc	agg	tat	ata	ctg	gag	ata	act	gga	aag	gac	gga	ttg	2237
198	Lys	Asp	Arg	Ser	Arg	Tyr	Ile	Leu	Glu	Ile	Thr	Gly	Lys	Asp	Gly	Leu	
199		680					685					690					
201	ata	ctg	ttc	caa	aca	ctc	att	gga	ttc	atc	agt	gaa	aga	aag	aac	gct	2285
202	Ile	Leu	Phe	Gln	Thr	Leu	Ile	Gly	Phe	Ile	Ser	Glu	Arg	Lys	Asn	Ala	
203	695				700					705						710	
205	ctg	ctt	aat	aag	gca	ata	tct	cag	agg	gaa	atg	aac	aac	ttg	gaa	aac	2333
206	Leu	Leu	Asn	Lys	Ala	Ile	Ser	Gln	Arg	Glu	Met	Asn	Asn	Leu	Glu	Asn	
207				715					720					725			
209	aat	gga	ttt	tac	agg	ctc	agt	gaa	ttc	aat	gtc	agc	acg	gaa	tac	tat	2381
210	Asn	Gly	Phe	Tyr	Arg	Leu	Ser	Glu	Phe	Asn	Val	Ser	Thr	Glu	Tyr	Tyr	
211			730					735					740				
213	gag	ggc	aag	gtc	tat	gac	tta	act	ctt	gaa	gga	act	ccc	tac	tac	ttt	2429
214	Glu	Gly	Lys	Val	Tyr	Asp	Leu	Thr	Leu	Glu	Gly	Thr	Pro	Tyr	Tyr	Phe	
215			745					750					755				
217	gcc	aat	ggc	ata	ttg	acc	cat	aac	tcc	ctg	tac	ccc	tca	atc	atc	atc	2477
218	Ala	Asn	Gly	Ile	Leu	Thr	His	Asn	Ser	Leu	Tyr	Pro	Ser	Ile	Ile	Ile	
219		760					765					770					
221	acc	cac	aac	gtc	tcg	ccg	gat	acg	ctc	aac	aga	gaa	gga	tgc	aag	gaa	2525
222	Thr	His	Asn	Val	Ser	Pro	Asp	Thr	Leu	Asn	Arg	Glu	Gly	Cys	Lys	Glu	
223	775					780				785						790	
225	tat	gac	gtt	gcc	cca	cag	gtc	ggc	cac	cgc	ttc	tgc	aag	gac	ttc	cca	2573
226	Tyr	Asp	Val	Ala	Pro	Gln	Val	Gly	His	Arg	Phe	Cys	Lys	Asp	Phe	Pro	
227				795					800					805			
229	gga	ttt	atc	ccg	agc	ctg	ctt	gga	gac	ctc	cta	gag	gag	agg	cag	aag	2621
230	Gly	Phe	Ile	Pro	Ser	Leu	Leu	Gly	Asp	Leu	Leu	Glu	Glu	Arg	Gln	Lys	
231			810					815					820				
233	ata	aag	aag	aag	atg	aag	gcc	acg	att	gac	ccg	atc	gag	agg	aag	ctc	2669
234	Ile	Lys	Lys	Lys	Met	Lys	Ala	Thr	Ile	Asp	Pro	Ile	Glu	Arg	Lys	Leu	
235			825					830					835				
237	ctc	gat	tac	agg	cag	agg	gcc	atc	aag	atc	ctg	gca	aac	agc	atc	cta	2717
238	Leu	Asp	Tyr	Arg	Gln	Arg	Ala	Ile	Lys	Ile	Leu	Ala	Asn	Ser	Ile	Leu	
239		840					845					850					
241	ccc	gag	gaa	tgg	ctt	cca	gtc	ctc	gag	gaa	ggg	gag	gtt	cac	ttc	gtc	2765
242	Pro	Glu	Glu	Trp	Leu	Pro	Val	Leu	Glu	Glu	Gly	Glu	Val	His	Phe	Val	
243	855					860				865						870	
245	agg	att	gga	gag	ctc	ata	gac	cgg	atg	atg	gag	gaa	aat	gct	ggg	aaa	2813
246	Arg	Ile	Gly	Glu	Leu	Ile	Asp	Arg	Met	Met	Glu	Glu	Asn	Ala	Gly	Lys	
247				875					880					885			
249	gta	aag	aga	gag	ggc	gag	acg	gaa	gtg	ctt	gag	gtc	agt	ggg	ctt	gaa	2861
250	Val	Lys	Arg	Glu	Gly	Glu	Thr	Glu	Val	Leu	Glu	Val	Ser	Gly	Leu	Glu	

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251		890		895		900		
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254	Val	Pro	Ser	Phe	Asn	Arg	Arg	Thr
255		905		910		915		
257	aag	gcc	ctg	att	agg	cac	gat	tat
258	Lys	Ala	Leu	Ile	Arg	His	Asp	Tyr
259		920		925		930		
261	ctg	aag	tcg	ggg	agg	aga	ata	aag
262	Leu	Lys	Ser	Gly	Arg	Arg	Ile	Lys
263	935			940		945		950
265	tct	gtg	aga	aac	ggg	gag	ctc	gtt
266	Ser	Val	Arg	Asn	Gly	Glu	Leu	Val
267				955		960		965
269	cca	ggt	gac	ctc	gtt	gca	gtc	ccg
270	Pro	Gly	Asp	Leu	Val	Ala	Val	Pro
271				970		975		980
273	aac	cac	gtg	ctg	aac	ctc	gtt	gaa
274	Asn	His	Val	Leu	Asn	Leu	Val	Glu
275				985		990		995
277	gaa	act	ttg	gac	atc	gtc	atg	acg
278	Glu	Thr	Leu	Asp	Ile	Val	Met	Thr
279		1000			1005			1010
281	ttc	ttt	aaa	ggg	atg	ctc	agg	act
282	Phe	Phe	Lys	Gly	Met	Leu	Arg	Thr
283	1015				1020			1025
285	aag	agg	ccc	aga	acc	gcg	aga	cgc
286	Lys	Arg	Pro	Arg	Thr	Ala	Arg	Arg
287				1035				1040
289	ggc	tat	gtc	cgg	ctt	aag	aag	atc
290	Gly	Tyr	Val	Arg	Leu	Lys	Lys	Ile
291				1050				1055
293	tca	ctt	aag	aac	tac	aga	agg	ctc
294	Ser	Leu	Lys	Asn	Tyr	Arg	Arg	Leu
295				1065				1070
297	aga	tac	aac	ggc	aac	aag	agg	gag
298	Arg	Tyr	Asn	Gly	Asn	Lys	Arg	Glu
299		1080			1085			1090
301	cgg	gat	gca	gtt	ggc	ata	atg	ccc
302	Arg	Asp	Ala	Val	Gly	Ile	Met	Pro
303	1095				1100			1105
305	atc	ggc	acg	ctg	aac	ggc	ttc	aga
306	Ile	Gly	Thr	Leu	Asn	Gly	Phe	Arg
307				1115				1120
309	gag	tcg	tta	gca	aag	ctc	ctc	ggc
310	Glu	Ser	Leu	Ala	Lys	Leu	Leu	Gly
311				1130				1135
313	aga	aag	cag	agg	aat	ccc	aaa	aac
314	Arg	Lys	Gln	Arg	Asn	Pro	Lys	Asn
315				1145				1150

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L:5 M:283 W: Missing Blank Line separator, <140> field identifier
L:9 M:283 W: Missing Blank Line separator, <160> field identifier
L:11 M:283 W: Missing Blank Line separator, <210> field identifier
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